IN THE CLAIMS

1. (amended) A method for predicting biomolecular interactions comprising,

inputting a first set of biomolecules into a trainable system, wherein the first set comprises primary structures of a training set ~~primary structure~~ of biomolecules with known interactions, and the trainable system comprises a support vector learning machine ~~comprising into a trainable system~~,

teaching the trainable system using known interaction domains between members of the first set of biomolecules and assign a value for binding of the interaction domains to each other, wherein the binding of the domains is indicated by a minimum threshold value,

inputting a second set of biomolecules into the trainable system, wherein the second set comprises primary structures of a set of biomolecules with unknown interactions ~~into the trainable system~~, and

predicting interactions between members of the second set of biomolecules ~~with unknown interactions~~ by analyzing at least one fragment of a first biomolecule of the second set and assigning a value for binding to at least one fragment of a second biomolecule of the second set and assigning a value for binding of the first fragment to the second fragment wherein binding is indicated by a value at least equal to the minimum threshold value ~~by analogy to the biomolecules in the training set using the trainable system~~.

2. (original) The method of claim 1, wherein the interactions are homotypic.

3. (original) The method of claim 1, wherein the interactions are heterotypic.

4. (original) The method of claim 1, wherein the biomolecule is a protein.

5. (original) The method of claim 1, wherein the biomolecule is a nucleic acid.

6. (original) The method of claim 1, wherein the biomolecule is a bioactive agent.

7. (cancelled)

8. (amended) A trainable system for predicting biomolecular interactions comprising,

a training set comprising primary structure of a first set of biomolecules with known interactions ~~into a trainable system~~,

an algorithm for quantifying interactions between biomolecules known to interact,

a set of biomolecules with unknown interactions wherein the biomolecules are represented as a linear set of features ~~into the trainable system~~, ~~and~~

a system for predicting interactions between members of the set of biomolecules with unknown interactions wherein the system performs a series of pairwise comparisons between each biomolecule of the training set with each biomolecule of the unknown interaction set and predicts interaction between the biomolecules of the unknown interaction set by analogy to the biomolecules in the training set ;and

the trainable system comprises a support vector learning machine.

9. (new) The method of claim 1, wherein the training set further comprises pairs of biomolecules known to not interact.

10. (new) A method for predicting biomolecular interactions comprising:

a) inputting a set of biomolecules with known interactions into a trainable system, wherein each biomolecules comprises a series of features ;

b) representing the biomolecules by data vectors of features wherein the features comprise primary structure of the biomolecules and associated

physicochemical properties of each element of the primary structure in sequence;

c) assembling paired sets of features to allow comparison of the features to each other;

d) training the trainable system using a deterministic optimization algorithm by introducing pairs of known interactions and labels indicating a positive interaction status to develop a pattern recognition system;

e) optimizing the pattern recognition system by performing a systematic computational search over a range of model parameters;

f) inputting features of biomolecules with unknown interactions into the trained system;

g) predicting labels of biomolecules with unknown interaction status by using the trained system;

h) estimating statistical confidence in the predictions using cross validation errors obtained in the optimization process.

11. (new) The method of Claim 1, wherein the interactions are homotypic.

12. (new) The method of Claim 1, wherein the interactions are heterotypic.

13. (new) The method of Claim 1, wherein at least one biomolecule is a protein.

14. (new) The method of Claim 1, wherein at least one biomolecule is a nucleic acid.

15. (new) The method of Claim 1, wherein at least one biomolecule is a bioactive agent.

16. (new) The method of Claim 1, wherein the trainable system is a support vector machine (SVM) comprising:

a) a collection of support vectors identified during an optimization process to define boundaries of a statistical decision surface used to discriminate input features;

b) a linear combination of these support vectors;

c) parameters defining the location and orientation of the decision surface in high-dimensional feature space; and

d) an analytical upper bound on the generalization error associated with a set of novel features input to the trained SVM.

17. (new) The method of Claim 1, wherein the training set further comprises pairs of biomolecules known to not interact.

18. (new) The method of Claim 1, wherein the set of biomolecules is from a complete genome.